

FIGURE 1

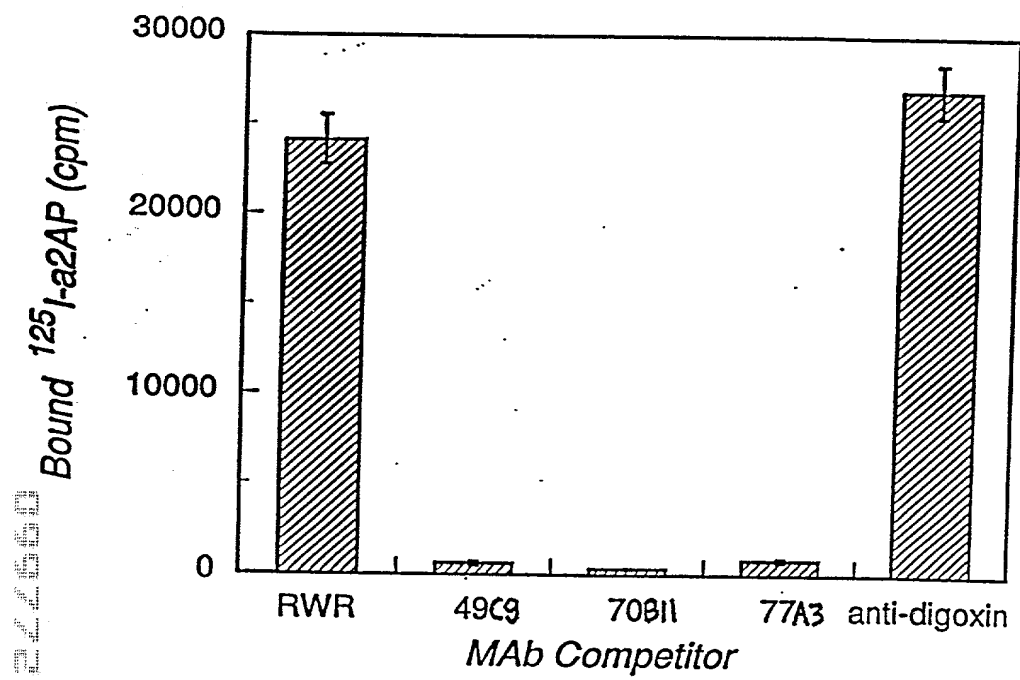


FIGURE 2

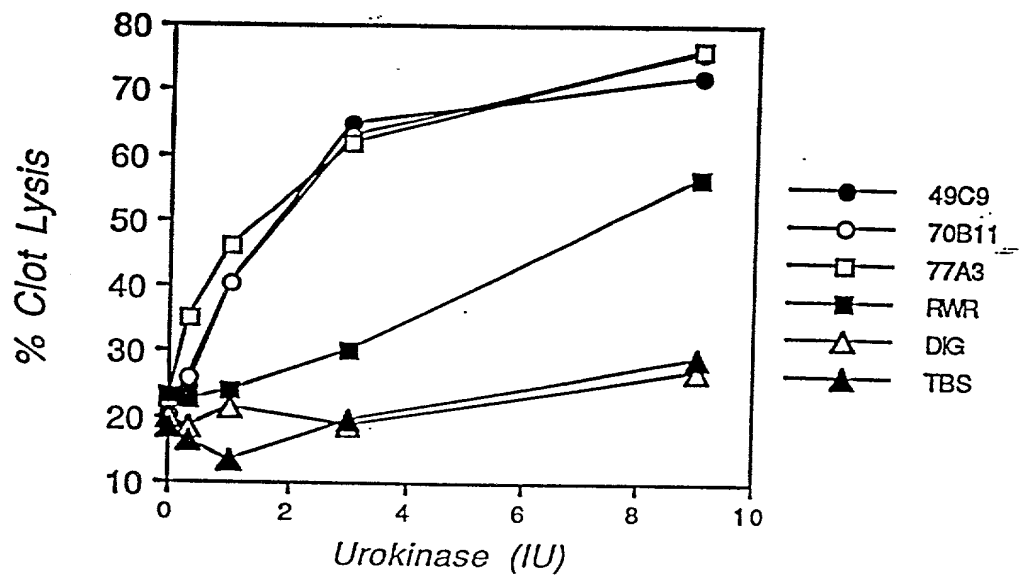


FIGURE 3

TOP SECRET 00000000

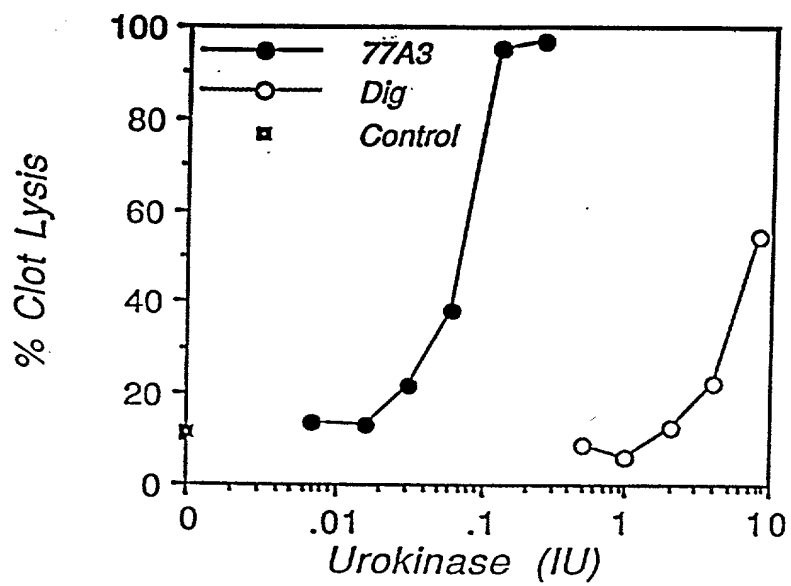
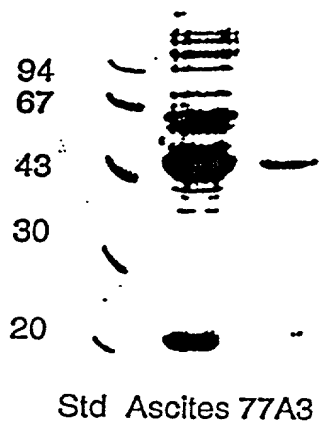


FIGURE 4



**FIGURE 5**



199701 0024650

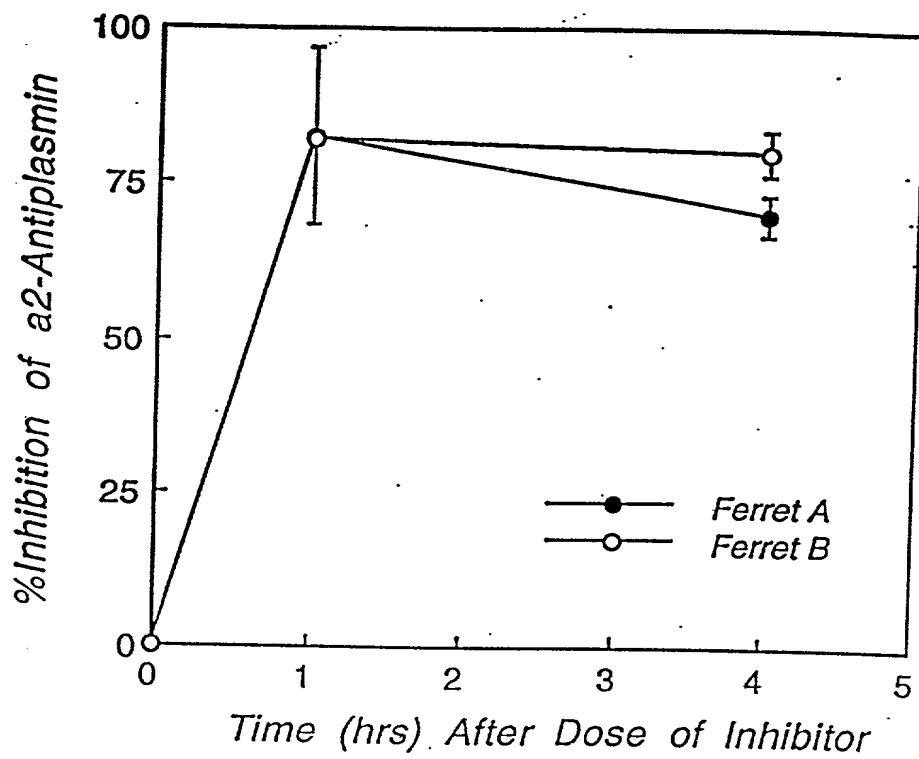


FIGURE 7

209707 29272650

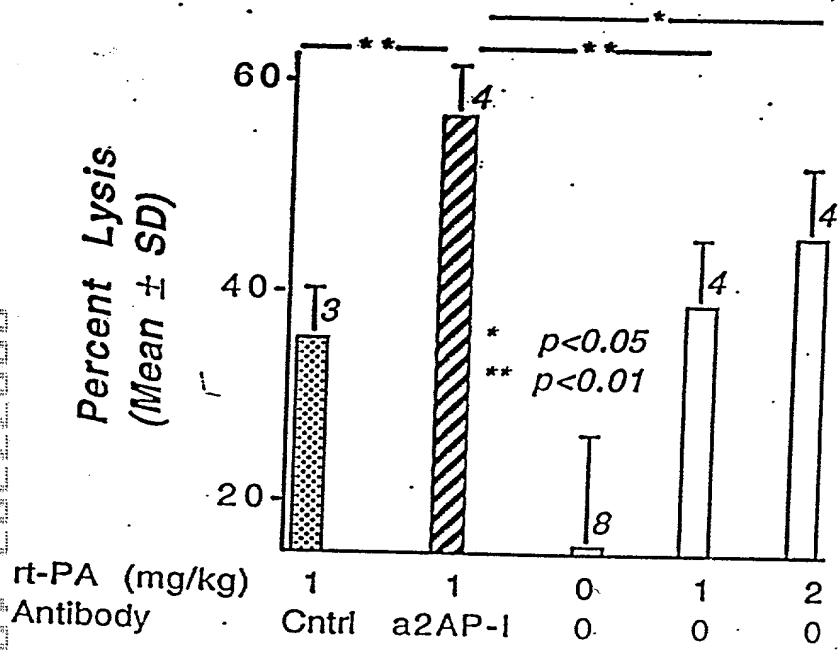


FIGURE 8



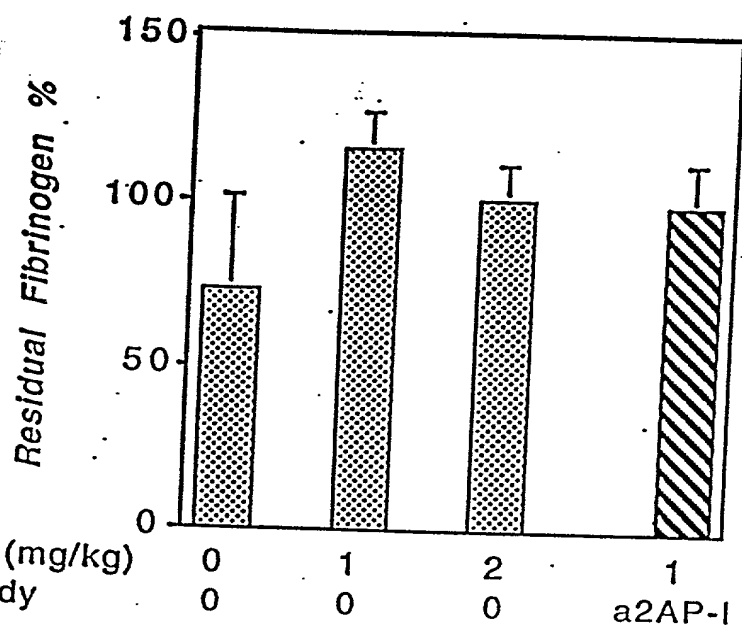


FIGURE 9

Fig. 10

MAb Light Chain	Amino Terminal Sequence
49C9	xIQMTQSPASLSASV
70B11	DIQMT
77A3	xIQMTQSPASLSASV

1990-1991-1992-1993-1994-1995-1996-1997-1998-1999-2000-2001-2002-2003-2004-2005-2006-2007-2008-2009-2010-2011-2012-2013-2014-2015-2016-2017-2018-2019-2020-2021-2022-2023-2024-2025

[illegible]

10	20	30	40	50	60
*	*	G	*	*	*
ATGAGTGTGC	TCACTCAGGT	CCTGGCGTTG	CTGCTGCTGT	GGCTTACAGG	TGCCAGATGT
M S V	L T Q V	L G L	L L L	W L T G	A R C>
		A			
70	80	90	100	110	120
*	*	*	*	*	*
GACATCCAGA	TGACTCAGTC	TCCAGCCTCC	CTATCTGCAT	CTGTGGGAGA	AACTGTCACC
D I Q	M T Q S	P A S	L S A	S V G E	T V T>
130	140	150	160	170	180
*	*	*	*	*	*
ATCACATGTC	GAGCAAGTGG	GAATATTCAC	AATTATTTAG	CATGGTATCA	GCAGAAACAG
I T C	R A S G	N I H	N Y L	A W Y Q	Q K Q>
190	200	210	220	230	240
*	*	*	*	*	*
GGAAAATCTC	CTCAGCTCCT	GGTCTATAAT	GCAAAAACCT	TAGCAGATGG	TGTGCCATCA
G K S	P Q L L	V Y N	A K T	L A D G	V P S>
250	260	270	280	290	300
*	*	*	*	*	*
AGGTTTCAGTG	GCAGTGGATC	AGGAACACAA	TTTTCTCTCA	GGATCAACAG	CCTGCAGCCT
R F S	G S G S	G T Q	F S L	R I N S	L Q P>
310	320	330	340	350	360
*	*	*	*	*	*
GAAGATTTTG	GGAGTCATTA	CTGTCAACAT	TTTTGGACCA	CTCCGTGGAC	GTTCGGTGG A
E D F	G S H Y	C Q H	F W T	T P W T	F G G>
370	380				
*	*				
GGCACCAAGC	TGGAAATCAA	A			
G T K	L E I K				

Fig. 12

10	20	30	40	50	60
*	*	*	*	*	*
ATGAGTGTGC TCACTCAGGT CCTGGGGTTG CTGCTGCTGT GGCTTACAGG TGCCAGATGT					
M	S	V	L	T	Q
V	L	G	L	L	L
W	L	T	G	A	R
C>					
70	80	90	100	110	120
*	*	*	*	*	*
GACATCCAGA TGA CTCAGTC TCCAGCCTCC CTATCTGCAT CTGTGGGAGA AACTGTCACC					
D	I	Q	M	T	Q
S	P	A	S	L	S
A	S	V	G	E	T
V	T>				
130	140	150	160	170	180
*	*	*	*	*	*
GTCACATGTC GAGCAAGTGG GAATATTCAC AATTATTTAG CATGGTATCA GCAGAAACAG					
V	T	C	R	A	S
G	N	I	H	N	Y
L	A	W	Y	Q	Q
K	Q>				
190	200	210	220	230	240
*	*	*	*	*	*
GGAAAATCTC CTCAGCTCCT GGTCTATAAT GCAAGAACCT TAGCAGATGG TGTGCCATCA					
G	K	S	P	Q	L
L	V	Y	N	A	R
T	L	A	D	G	V
P	S>				
250	260	270	280	290	300
*	*	*	*	*	*
AGGTTTCAGTG GCAGTGGATC AGGAACACAA TATTCTCTCA AGATCAACAG CCTGCAGCCT					
R	F	S	G	S	G
S	G	T	Q	Y	S
L	K	I	N	S	L
Q	P>				
310	320	330	340	350	360
*	*	*	*	*	*
GAAGATTTTG GGAGTTATTA CTGTCAACAT TTTTGGAGTA ATCCGTGGAC GTTCGGTGG					
E	D	F	G	S	Y
Y	C	Q	H	F	W
S	N	P	W	T	F
G	G>				
370	380				
*	*				
GGCACCAAGC TGGAAATCAA					
G	T	K	L	E	I
K					

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Fig. 13

10	20	30	40	50	60
*	*	*	*	*	*
ATGAGTGTGC TCACTCAGGT CCTGGCGTTG CTGCTGCTGT GGCTTACAGG TGCCAGATGT					
M S V L T Q V L A L L L L W L T G A R C>					
70	80	90	100	110	120
*	*	*	*	*	*
GACATCCAGA TGACTCAGTC TCCAGCCTCC CTATCTGCAT CTGTGGGAGA AACTGTCACC					
D I Q M T Q S P A S L S A S V G E T V T>					
130	140	150	160	170	180
*	*	*	*	*	*
ATCACATGTC GAGCAAGTGG GAATATTCAC AATTATTTAG CATGGTATCA GCAGAAACAG					
I T C R A S G N I H N Y L A W Y Q Q K Q>					
190	200	210	220	230	240
*	*	*	*	*	*
GGAAAATCTC CTCAACTCCT GGTCTATAAT GCAAAAACCT TAGCAGATGG TGTGCCATCA					
G K S P Q L L V Y N A K T L A D G V P S>					
250	260	270	280	290	300
*	*	*	*	*	*
AGGTTTCAGTG GCAGTGGATC AGGAACACAA TTTTCTCTCA AGATCAACAG CCTGCAGCCT					
R F S G S G S G T Q F S L K I N S L Q P>					
310	320	330	340	350	360
*	*	*	*	*	*
GAAGATTTTG GGAGTCATTA CTGTCAACAT TTTTGGACCA CTCCGTGGAC GTTCGGTGGA					
E D F G S H Y C Q H F W T T P W T F G G>					
370	380				
*	*				
GGCACCAAGC TGGAAATCAA A					
G T K L E I K					

6577653 40504

H2 HC (49c9 heavy chain) Fig. 14

```

      9      19      29      39      49      59
      *      *      *      *      *      *
ATGGMTTGG GTGTGGAMCT TGCTATTCCCT GATGGCAGCT GCCCAAAGTC TCCAAGCACA
M A W V W N L L F L M A A A Q S L Q A Q>
      D      T

      69      79      89      99      109      119
      *      *      *      *      *      *
GATCCAGTTG GTGCAGTCTG GACCTGAGCT GAAGAAGCCT GGAGAAACAG TCAAGATCTC
I Q L V Q S G P E L K K P G E T V K I S>

      129      139      149      159      169      179
      *      *      *      *      *      *
CTGCAAGGCC TCTGGGTATA CCTTCACAAA CTATGGAATG AACTGGGTGA AGCAGGCTCC
C K A S G Y T F T N Y G M N W V K Q A P>

      189      199      209      219      229      239
      *      *      *      *      *      *
AGGAAAGGGT TTAAAGTGGA TGGGCTGGAT AAACACCAAG AGTGGAGAGC CAACATATGC
G K G L K W M G W I N T K S G E P T Y A>

      249      259      269      279      289      299
      *      *      *      *      *      *
TGAAGAGTTC AAGGGACGGT TTGTCTTCTC TTTGGAAACC TCTGCCAGCA CTGCCCATT
E E F K G R F V F S L E T S A S T A H L>

      309      319      329      339      349      359
      *      *      *      *      *      *
GCAGATCAAG AATTTTCAGAA ATGAGGACAC GGCTACATAT TTCTGTGCAA GATGGGTACC
Q I K N F R N E D T A T Y F C A R W V P>

      369      379      389      399      409
      *      *      *      *      *
TGGGACCTAT GCTATGGACT ACTGGGGTCA AGGAACCTCA GTCACCGTCT CCTCA
G T Y A M D Y W G Q G T S V T V S S>

```

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H3 HC (70B11 heavy chain) Fig. 15

10	20	30	40	50	60
*	*	*	*	*	*
ATGGM	TTGGG	TGTGG	AMCTT	GCTATT	CCTG
M	A	W	V	W	N
					L
					L
					F
					L
					M
					A
					A
					A
					Q
					S
					I
					Q
					A
					Q
					>
70	80	90	100	110	120
*	*	*	*	*	*
ATCCAG	TTGG	TGCAG	TCTGG	ACCTG	AGCTG
I	Q	L	V	Q	S
					G
					P
					E
					L
					K
					K
					P
					G
					E
					T
					V
					K
					I
					S
					>
130	140	150	160	170	180
*	*	*	*	*	*
TGCAAG	GCTT	CTGGG	TATAC	CTTCAC	AAAG
C	K	A	S	G	Y
					T
					F
					T
					K
					Y
					G
					M
					N
					W
					V
					K
					Q
					A
					P
					>
190	200	210	220	230	240
*	*	*	*	*	*
GGAAAG	GGGT	TAAAG	TGGAT	GGGCT	GGATA
G	K	G	L	K	W
					M
					G
					W
					I
					N
					T
					N
					S
					G
					E
					P
					T
					Y
					A
					>
250	260	270	280	290	300
*	*	*	*	*	*
GAAGAG	TTCA	AGGGAC	GGTT	TGCCTT	CTCT
E	E	F	K	G	R
					F
					A
					F
					S
					L
					E
					T
					S
					A
					S
					T
					A
					Y
					L
					>
310	320	330	340	350	360
*	*	*	*	*	*
CAGATC	CAACA	ACCTCA	AAAAA	TGAGGA	CTCG
Q	I	N	N	L	K
					N
					E
					D
					S
					A
					T
					Y
					F
					C
					A
					R
					W
					V
					P
					>
370	380	390	400	410	
*	*	*	*	*	
GGGAC	CTATG	GACTA	CTGGG	GTCAA	
G	T	Y	A	M	D
					Y
					W
					G
					Q
					G
					T
					S
					V
					T
					V
					S
					S
					>

6577663-44604

H4 HC (77A3 heavy chain) Fig. 16

10	20	30	40	50	60
*	*	*	*	*	*
ATGGMTTGGG	TGTGGAMCTT	GCTATTCCTG	ATGGCAGCTG	CCCAAAGTAT	CCAAGCACAG
M A W	V W N L	L F L	M A A	A Q S I	Q A Q>
D	T				
70	80	90	100	110	120
*	*	*	*	*	*
ATCCAGTTGG	TGCAGTCTGG	ACCTGAGCTG	AAGAAGCCTG	GAGAAACAGT	CAAGATCTCC
I Q L	V Q S G	P E L	K K P	G E T V	K I S>
130	140	150	160	170	180
*	*	*	*	*	*
TGCAAGGCTT	CTGGGTATAC	CTTCACAAAC	TATGGAATGA	ACTGGGTGAA	GCAGGCTCCA
C K A	S G Y T	F T N	Y G M	N W V K	Q A P>
190	200	210	220	230	240
*	*	*	*	*	*
GGAAAGGGTT	TAAAGTGGAT	GGGCTGGATA	AACACCAAGA	GTGGAGAGCC	AACATATGCT
G K G	L K W M	G W I	N T K	S G E P	T Y A>
250	260	270	280	290	300
*	*	*	*	*	*
GAAGAGTTCA	AGGGACGGTT	TGCCTTCTCT	TTGGAAACCT	CTGCCAGCAC	TGCCAATTTG
E E F	K G R F	A F S	L E T	S A S T	A N L>
310	320	330	340	350	360
*	*	*	*	*	*
CAGATCAAGA	ACCTCAAAAA	TGAGGACACG	GCTACATATT	TCTGTGCAAG	ATGGGTACCT
Q I K	N L K N	E D T	A T Y	F C A R	W V P>
370	380	390	400	410	
*	*	*	*	*	
GGGACCTATG	CCATGGACTA	CTGGGGTCAA	GGAACCTCAG	TCACCGTCTC	CTCA
G T Y	A M D Y	W G Q	G T S	V T V S	S

109707 0922659  
0922659 404604



Figure 17

## h77A3v L

Humanized nt (sense)

12221  
 222110987654321  
 M S V L T Q V L A L L L L W L T G A R C  
 A T G A C T G T G C T C A C G C C T G C C C T T G C C G T T A C A G T T G C C A C A T C T  
 T A C T C A C A C G A G T C C A G C A C C G C C A C G C C A C C G G T C C A C C G G T T T A C A

# h77A3VL

Humanized nt (sense)

[illegible]

h77A3v2

Humanized nt (sense)

[illegible]

## h77A3v2

Humanized nt (sense)

7 5	I S L Q P E D F G S H Y C Q H T P	8 0	9 0	9 5	a b c d e f	9 8	W	T F G G T K L E I	1 0 0 6 8 a	1 0 0 7										
ATC	AGC	ACC	CTG	CAG	CCT	GAA	GAT	TTT	CGG	ACT	CAT	TAC	TGT	GAA	CTT	ACC	CTT	GTA	ATC	AAA
TAG	TGG	TGG	CAC	GTC	GAA	CTT	GTA	ATG	ACG	CTT	GTA	ATG	ACG	CTT	GTA	ATG	ACG	CTT	GTA	ATG

[illegible]

Figure 18

## Signal Peptide

[illegible]

Humanized (aa)  
Humanized nt (sense)  
Humanized nt (anti-sense)

## H1 Loop

NO

FO

Humanized (aa)  
Humanized nt (sense)  
Humanized nt (anti-sense)

H2 Loop

4	5	5
4	0	2

Humanized (aa)  
Humanized nt (sense)  
Humanized nt (anti-sense)

### H3 Loop

94  
2  
90  
63

Humanized (aa)  
Humanized nt (sense)  
Humanized nt (anti-sense)

Y	A	M	D	Y	W	Q	G	T	T	V	T	V	S	S
TAT	GCT	ATG	GAC	TAC	TGG	GCT	CAG	ACC	ACG	GTC	ACC	GTC	TCC	TCA
ATA	CGG	TAC	CTG	ATG	ACT	GCA	GCT	GCT	TGG	TGC	CAG	TGG	CAG	AGG

K	K	A	E	D	T	A	V	F	C	A	R	W	P	G	T
TTT	CGA	ACC	GAG	ACC	GCT	GTC	TAT	TTC	TGT	GCA	AGA	TGG	GTA	GCT	GGG
TTT	CGA	GTC	GTC	TGC	GCA	CAC	ATA	AGC	ACA	GCT	TCT	ACC	CAT	GCA	CCC

## Signal Peptide

Humanized (aa)  
Humanized nt (sense)  
Humanized nt (anti-sense)

[illegible]

CGA TTG GAA TTC TTG CCG CCG CTT GCT AGC

Humanized (aa)  
Humanized nt (sense)  
Humanized nt (anti-sense)

[illegible]

## H1 Loop

## H2 Loop

Humanized (aa)  
Humanized nt (sense)  
Humanized nt (anti-sense)

[illegible]

### H3 Loop

Humanized (aa)  
Humanized nt (sense)  
Humanized nt (anti-sense)[illegible]

Figure 20

Plasmin Assay  
Murine, Chimeric and Humanized 77A3

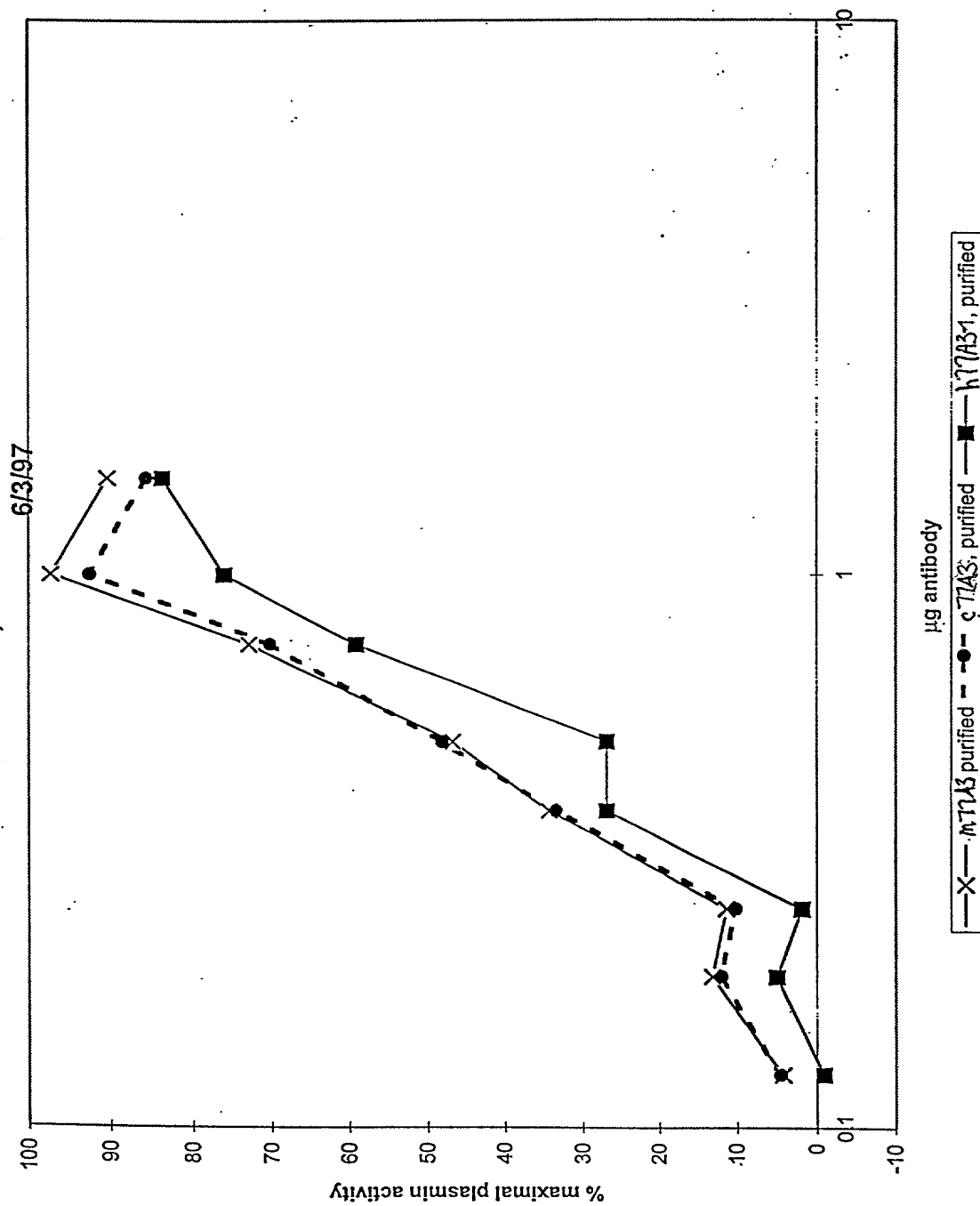


Figure 21

# $\alpha$ 2-antiplasmin antibody light chain sequences

77A3-1 and h77A3-2

h77A3-1 and h77A3-2  
m77A3  
m49C9  
m70B11  
murine consensus  
77A3/49C9 consensus  
all

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18																
h77A3-1 and h77A3-2	D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	A	S	G	N	I	H	N	Y	L	A
m77A3	D	I	Q	M	T	Q	S	P	A	S	L	S	A	S	V	G	E	T	V	T	I	T	C	R	A	S	G	N	I	H	N	Y	L	A
m49C9	D	I	Q	M	T	Q	S	P	A	S	L	S	A	S	V	G	E	T	V	T	I	T	C	R	A	S	G	N	I	H	N	Y	L	A
m70B11	D	I	Q	M	T	Q	S	P	A	S	L	S	A	S	V	G	E	T	V	T	V	T	C	R	A	S	G	N	I	H	N	Y	L	A
murine consensus	D	I	Q	M	T	Q	S	P	A	S	L	S	A	S	V	G	E	T	V	T	X	T	O	R	A	S	G	N	I	H	N	Y	L	A
77A3/49C9 consensus	D	I	Q	M	T	Q	S	P	A	S	L	S	A	S	V	G	E	T	V	T	I	T	C	R	A	S	G	N	I	H	N	Y	L	A
all	D	I	Q	M	T	Q	S	P	X	S	L	S	A	S	V	G	X	X	V	T	X	T	C	R	A	S	G	N	I	H	N	Y	L	A

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18																						
h77A3-1 and h77A3-2	W	Y	Q	Q	K	Q	G	K	S	P	Q	L	L	V	Y	N	A	K	T	L	A	S	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T
m77A3	W	Y	Q	Q	K	Q	G	K	S	P	Q	L	L	V	Y	N	A	K	T	L	A	D	G	V	P	S	R	F	S	G	S	G	S	G	T	Q	F	S	L	K
m49C9	W	Y	Q	Q	K	Q	G	K	S	P	Q	L	L	V	Y	N	A	K	T	L	A	D	G	V	P	S	R	F	S	G	S	G	S	G	T	Q	F	S	L	R
m70B11	W	Y	Q	Q	K	Q	G	K	S	P	Q	L	L	V	Y	N	A	R	T	L	A	D	G	V	P	S	R	F	S	G	S	G	S	G	T	Q	Y	S	L	K
murine consensus	W	Y	Q	Q	K	Q	G	K	S	P	Q	L	L	V	Y	N	A	X	T	L	A	D	G	V	P	S	R	F	S	G	S	G	S	G	T	Q	X	S	L	X
77A3/49C9 consensus	W	Y	Q	Q	K	Q	G	K	S	P	Q	L	L	V	Y	N	A	K	T	L	A	D	G	V	P	S	R	F	S	G	S	G	S	G	T	Q	F	S	L	X
all	W	Y	Q	Q	K	Q	G	K	S	P	Q	L	L	V	Y	N	A	X	T	L	A	X	G	V	P	S	R	F	S	G	S	G	S	G	T	X	X	X	L	X

h77A3-1 and h77A3-2  
m77A3  
m49C9  
m70B11  
murine consensus  
77A3/49C9 consensus  
all

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18															
h77A3-1 and h77A3-2	I	S	S	L	Q	P	E	D	F	G	S	H	Y	C	Q	H	F	W	T	T	P	W	T	F	G	G	G	T	K	L	E	I	K
m77A3	I	N	S	L	Q	P	E	D	F	G	S	H	Y	C	Q	H	F	W	T	T	P	W	T	F	G	G	G	T	K	L	E	I	K
m49C9	I	N	S	L	Q	P	E	D	F	G	S	H	Y	C	Q	H	F	W	T	T	P	W	T	F	G	G	G	T	K	L	E	I	K
m70B11	I	N	S	L	Q	P	E	D	F	G	S	Y	Y	C	Q	H	F	W	S	N	P	W	T	F	G	G	G	T	K	L	E	I	K
murine consensus	I	N	S	L	Q	P	E	D	F	G	S	X	Y	C	Q	H	F	W	X	X	P	W	T	F	G	G	G	T	K	L	E	I	K
77A3/49C9 consensus	I	N	S	L	Q	P	E	D	F	G	S	H	Y	C	Q	H	F	W	T	T	P	W	T	F	G	G	G	T	K	L	E	I	K
all	I	X	S	L	Q	P	E	D	F	G	S	X	Y	C	Q	H	F	W	X	X	P	W	T	F	G	G	G	T	K	L	E	I	K

Figure 22

 $\alpha$ 2-antiplasmin antibody heavy chain sequences

		H1 Loop									
		1	2	3	4	5	6	7	8	9	10
h77A3-1	QIQLVQSGSELKKPGASVKISCKAS	G	Y	T	F	T	N	Y	G	M	N
h77A3-2	QIQLVQSGAEVKKPGASVKISCKAS	G	Y	T	F	T	N	Y	G	M	N
m77A3	QIQLVQSGPELKKPGGETVKISCKAS	G	Y	T	F	T	N	Y	G	M	N
m49C9	QIQLVQSGPELKKPGGETVKISCEAS	G	Y	T	F	T	N	Y	G	M	N
m70B11	QIQLVQSGPELKKPGGETVKISCKAS	G	Y	T	F	T	K	Y	G	M	N
humanized consensus	QIQLVQSGXEXKKPGASVKISCKAS	G	Y	T	F	T	N	Y	G	M	N
murine consensus	QIQLVQSGPELKKPGGETVKISCXAS	G	Y	T	F	T	X	Y	G	M	N
77A3/49C9 consensus	QIQLVQSGPELKKPGGETVKISCXAS	G	Y	T	F	T	N	Y	G	M	N
all	QIQLVQSGXEXKKPGXXVKISCXAS	G	Y	T	F	T	X	Y	G	M	N

		H2 Loop									
		1	2	3	4	5	6	7	8	9	10
h77A3-1	GLEWMGWINT	K	S	G	E	P	T	A	E	E	F
h77A3-2	GLEWMGWINT	K	S	G	E	P	T	A	E	E	F
m77A3	GLKWMGWINT	K	S	G	E	P	T	A	E	E	F
m49C9	GLKWMGWINT	K	S	G	E	P	T	A	E	E	F
m70B11	GLKWMGWINT	N	S	G	E	P	T	A	E	E	F
humanized consensus	GLEWMGWINT	K	S	G	E	P	T	A	E	E	F
murine consensus	GLKWMGWINT	X	S	G	E	P	T	A	E	E	F
77A3/49C9 consensus	GLKWMGWINT	K	S	G	E	P	T	A	E	E	F
all	GLXWMGWINT	X	S	G	E	P	T	A	E	E	F

		H3 Loop									
		1	2	3	4	5	6	7	8	9	10
h77A3-1	KAEDTAVYFCARWVPGT	Y	A	M	D	Y	W	G	Q	G	T
h77A3-2	RSDDTAVYFCARWVPGT	Y	A	M	D	Y	W	G	Q	G	T
m77A3	KNEDTATYFCARWVPGT	Y	A	M	D	Y	W	G	Q	G	T
m49C9	RNEDTATYFCARWVPGT	Y	A	M	D	Y	W	G	Q	G	T
m70B11	KNEDSATYFCARWVPGT	Y	A	M	D	Y	W	G	Q	G	T
humanized consensus	XXXDTAVYFCARWVPGT	Y	A	M	D	Y	W	G	Q	G	T
murine consensus	XNEDXATYFCARWVPGT	Y	A	M	D	Y	W	G	Q	G	T
77A3/49C9 consensus	XNEDTATYFCARWVPGT	Y	A	M	D	Y	W	G	Q	G	T
all	XXXDXAXYFCARWVPGT	Y	A	M	D	Y	W	G	Q	G	T